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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/086,542

DATE: 03/19/2002 TIME: 14:47:56

Input Set : N:\Crf3\RULE60\10086542.raw
Output Set: N:\CRF3\03192002\J086542.raw

SEQUENCE LISTING

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(1) GENERAL INFORMATION:
            (i) APPLICANT: Wahl, Geoffrey M
                           O'Gorman, Stephen V
           (ii) TITLE OF INVENTION: FLP-MEDIATED GENE MODIFICATION IN
     6
                                    MAMMALIAN CELLS, AND COMPOSITIONS AND CELLS USEFUL
     8
     9
                                     THEREFOR
    10
          (iii) NUMBER OF SEQUENCES: 4
    12
           (iv) CORRESPONDENCE ADDRESS:
                 (A) ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
    14
    15
                 (B) STREET: 444 South Flower Street, Suite 2000
    16
                  (C) CITY: Los Angeles
    17
                  (D) STATE: California
                                                                  ENTERED
    18
                  (E) COUNTRY: USA
    19
                  (F) ZIP: 90071
    20
            (V) COMPUTER READABLE FORM:
    22
                  (A) MEDIUM TYPE: Floppy disk
    23
                  (B) COMPUTER: IBM PC compatible
    24
                  (C) OPERATING SYSTEM: PC-DOS/MS-DOS
                  (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
    25
     26
            (vi) CURRENT APPLICATION DATA:
     28
                  (A) APPLICATION NUMBER: US/10/086,542
C--> 29
                  (B) FILING DATE: 28-Feb-2002
C--> 30
                  (C) CLASSIFICATION:
     31
           (vii) PRIOR APPLICATION DATA:
     33
                  (A) APPLICATION NUMBER: 08/484,324
     34
                  (B) FILING DATE: 07-JUN-1995
     35
          (viii) ATTORNEY/AGENT INFORMATION:
     39
                  (A) NAME: Reiter, Stephen E
     40
                  (B) REGISTRATION NUMBER: 31,192
     41
                  (C) REFERENCE/DOCKET NUMBER: P41 9984
     42
            (ix) TELECOMMUNICATION INFORMATION:
     44
                  (A) TELEPHONE: (619) 546-4737
     45
                  (B) TELEFAX: (619) 546-9392
     46
     49 (2) INFORMATION FOR SEQ ID NO: 1:
             (i) SEQUENCE CHARACTERISTICS:
     51
                   (A) LENGTH: 1380 base pairs
     52
                   (B) TYPE: nucleic acid
     53
                   (C) STRANDEDNESS: single
     54
                   (D) TOPOLOGY: linear
      55
             (ii) MOLECULE TYPE: DNA (genomic)
      57
            (vii) IMMEDIATE SOURCE:
      60
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61

(B) CLONE: NATIVE FLP

PATENT APPLICATION: US/10/086,542

DATE: 03/19/2002 TIME: 14:47:56

(B) LOCATION: 11269 (8) (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1: 70 ATG CCA CAA TIT GAT ATA TATA TOT ANA ACA CCA CCT AAG GTG CTT GTT 70 ATG CCA CAA TIT GAT ATA TATA TOT ANA ACA CCA CCT AAG GTG CTT GTT 71 Met Pro Gln Phe Asp Ile Leu Cys Lys Thr Pro Pro Lys Val Leu Val 72 1 5 10 74 CGT CAG TIT GTG GAA AGG TIT GAA AGA CCT TCA GGT GAG AAA ATA GCA 75 Arg Gln Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys Ile Ala 76 20 78 TATA TGT GCT GGA CTA ACC TAT TATA TGT TGG ATG ATT ACA CAT AAC 79 Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys Trp Met Ile Thr His Asn 80 35 40 81 GGA ACA GCA ATC AAG AGA GCC ACA TTC ATG AGC TAT AAT ACT ATC ATA 81 Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr Asn Thr Ile Ile 83 Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr Asn Thr Ile Ile 84 50 86 AGC AAT TGG CTG AGT TTC GAT ATT GTC AAT AAA TCA CCC CAG TTT AAA 87 Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys Ser Leu Gln Phe Lys 88 65 90 TAC AAG AGG CAA AAA GCA ACA ATT CTG GAA GCC TCA TTA AAG AAA TTG 91 TYR Lys Thr Gln Lys Ala Thr Ile Leu Glu Ala Ser Leu Lys Lys Leu 91 Tyr Lys Thr Gln Lys Ala Thr Ile Leu Glu Ala Ser Leu Lys Lys Leu 92 65 94 ATT CCT GCT TGG GAA TTT ACA ATT ATT CCT TAC TAT TAG ACA AAA TTG 96 Ile Pro Ala Trp Glu Phe Thr Ile Ile Pro Tyr Tyr Gly Gln Lys His 100 115 102 TCA TCG GAA GAA GCA GAT ATA GGA ATT AGT AGT TG CAA TAAA CAG TTC GAA 97 GAA TGT GGT AGT ATC ACT GAT ATT GTA AGT TG CAA TAA CAG TTC GAA 103 Ser Ser Glu Glu Ala Asp Lys Gly Asn Ser His Ser Lys Lys Met Leu 101 15 102 TCA TCG GAA GAA GCA GAT AAG GGT GAA ACA ACT TGG GAA ATA CAG TTC 103 Ser Ser Glu Glu Ala Asp Lys Gly Asn Ser His Ser Lys Lys Met Leu 104 130 105 AAA GCA CTT CTA AGT GAG GGT GAA ACC ACT TGC GAA AAA CAT 107 Lys Ala Leu Leu Ser Phe Glu Tyr Thr Ser Arg Phe Thr Lys Thr 111 Ile Leu Asn Ser Phe Glu Tyr Thr Ser Arg Phe Thr Lys Thr 112 165 114 TTA TAC CAA TTC CTT TG GAT GAT ACT TGC AGA TTT AAA AAA AAA AAA 107 Lys Ala Leu Leu Ser Phe Glu Tyr Thr Ser Arg Phe Thr Lys Thr 119 Ser Asp Ile Lys Asn Val Asp Pro Lys Ser Phe Lys Leu Val Gln Asn 1	63 (ix) FEATURE: 64 (A) NAME/KEY: CDS	
68 (XI) SEQUENCE DESCRIPTION: SEQ ID NO. IT. 70 ATG CCA CAA TIT GAT ATA TITA TOT AAA ACA CCA CCT AAG GTG CTT GTT 70 ATG CCA CAA TITG GAT ATA TITA TOT AAA ACA CCA CCT AAG GTG CTT GTT 71 Met Pro Gln Phe Asp Ile Leu Cys Lys Thr Pro Pro Lys Val Leu Val 72 1 15 74 GGT CAG TIT GTG GAA AGG TIT GAA AGA CCT TCA GGT GAG AAA ATA GCA 75 Arg Gln Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys Ile Ala 76 20 78 TTA TGT GCT GCT GAA CTA ACC TAT TTA TGT TGG ATG ATT ACA CAT AAC 79 Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys Trp Met Ile Thr His Asn 40 35 60 35 60 ACA GCA ATC AAG AGA GCC ACA TCT ATG AGC TAT AAT ACT ATC ATA 83 Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr Asn Thr Ile Ile 63 GOA ACA GCA ATC AGA GAG GCC ACA TTC ATG AGC TAT AAT ACT ATC ATA 83 Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr Asn Thr Ile Ile 65 FO	(B) LOCATION: 11269	
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72 1 74 CGT CAG TTT GTG GAA AGG TTT GAA AGA CCT TCA GGT GAG AAA ATA GCA 75 Arg Gln Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys Ile Ala 76 20 778 TTA TGT GCT GCT GAA CTA ACC TAT TTA TGT TGG ATG ATT ACA CAT AAC 79 Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys Trp Met Ile Thr His Asn 80 35 80 40 81 GAA ACA GCA ATC AAG AGA GCC ACA TTC ATG AGC TAT AAT ACT ATA 83 Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr Asn Thr Ile Ile 84 50 85 6 AGC AAT TCG CTG GAT TTC GAT ATT GTG AGT AAAT ACA TCA TA 87 Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys Ser Leu Gln Phe Lys 87 Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys Ser Leu Gln Phe Lys 87 Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys Ser Leu Gln Phe Lys 88 65 90 95 91 Tyr Lys Thr Gln Lys Ala Thr Ile Leu Glu Ala Ser Leu Lys Lys Leu 91 Tyr Lys Thr Gln Lys Ala Thr Ile Leu Glu Ala Ser Leu Lys Lys Leu 91 Tyr Lys Thr Gln Lys Ala Thr Ile Ile Pro Tyr Tyr Gly Gln Lys His 110 105 92 AST 94 ATT CCT GCT GG AGA TTT ACA ATT ATT GTT ACT ACT ACT GAA AAA CAT 95 Ile Pro Ala Trp Glu Phe Thr Ile Ile Pro Tyr Tyr Gly Gln Lys His 100 105 96 100 105 97 115 102 TCA TCG GAA GAA GCA GAT AAG GGA AAT AGT GTT CAA TTA CAG TTC GAA 97 Gln Ser Asp Ile Thr Asp Ile Val Ser Ser Leu Gln Leu Gln Phe Glu 101 115 102 TCA TCG GAA GAA GCA GAT AAG GGA AAT AGC CAC AGT AAA AAA ACT 104 130 105 125 106 AAA GCA CTT CTA AGT GAG GGT GAA AGC ATC TG GAA ATA AGC ACT 107 Lys Ala Leu Leu Ser Glu Gly Ala ASP Lys Gly Asn Ser His Ser Lys Lys Met Leu 108 145 109 115 100 115 101 ATA CTA AAT TCG TTG GAG GGT GAA ACC ATC TG GAG ATT ACT GAG AAA 100 ATA CTA AAT TCG TTG GAG TAT ACT TG GAA ATT ACA AAT ACT ACT GAG AAA 101 ATA CTA AAT TCG TTG GAG TAT ACT TTC ACT TTC ACA ATT GTG GAA AAC 104 130 105 150 106 AAA GCA CTT CTA AGT GAG GGT GAA ACC ATC TCT ACT TTC ACA AAT ACA AAA ACC 107 Lys Ala Leu Leu Ser Glu Gly Try Thr Ser Arg Phe Thr Lys Thr Lys Thr 111 Ile Leu Asn Ser Phe Glu Tyr Thr Ser Arg Phe Thr Lys Thr 112 107 113 Ser Asp Ile Lys Asn val Asp Pro Lys Ser Phe Lys Leu Val Gln Asn 109 195 120 AG ACT ACT G	71 Met Pro Gln Phe Asp Ile Leu Cys Lys In 110 120 -1	
75 Arg Gln Phe Val 20 20 21 76 T20 20 21 76 T20 20 21 77 T20 78 TTA TGT GCT GCT GAA CTA ACC TAT TTA TGT TGG ATG ATT ACA CAT AAC 144 79 Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys Trp Met Ile Thr His Asn 45 80 35 40 45 81 GGA ACA GCA ATC AAG AGA GCC ACA TTC ATG AGC TAT AAT ACT ATC ATA 82 GGA ACA GCA ATC AAG AGA GCC ACA TTC ATG AGC TAT AAT ACT ATC ATA 83 Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr Asn Thr Ile Ile 84 50 55 60 86 AGC AAT TCG CTG AGT TTC GAT ATT GTC AAT AAA TCA CTC CAG TTT AAA 87 Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys Ser Leu Gln Phe Lys 88 65 70 90 TAC AAG ACG CAA AAA GCA ACA ATT CTG GAA GCC TCA TTA AAG AAA TTG 91 Tyr Lys Thr Gln Lys Ala Thr Ile Leu Glu Ala Ser Leu Lys Lys Leu 92 85 94 ATT CCT GCT TGG GAA TTT ACA ATT ATT CCT TAC TAT GGA CAA AAA CAT 95 Ile Pro Ala Trp Glu Phe Thr Ile Ile Pro Tyr Tyr Gly Gln Lys His 96 100 98 CAA TCT GAT ATC ACT GAT ATT GTA AGT AGT AGT AGA AAA ACA 99 Gln Ser Asp Ile Thr Asp Ile Val Ser Ser Leu Gln Phe Glu 105 100 115 102 TCA TCG GAA GAA GCA GAT ATG GAA AAT AGC CAC AGT AAAA AAA ACA 1336 106 AAA GCA CTT CTA AGT GAG GGT GAA AGC ATC TGG GAG ATC ACT GAG 107 Lys Ala Leu Leu Ser Glu Gly Glu Ser Ile Trp Glu Ile Thr Glu Lys 108 145 110 ATA CTA AAT TCG TT GAG TAT ACT TG AGA TTT CAA AAA ACA 111 Ile Leu Asn Ser Phe Glu Tyr Thr Ser Arg Phe Thr Lys Thr Lys Thr 111 Ile Leu Asn Ser Phe Glu Tyr Thr Ser Arg Phe Thr Lys Thr Lys Thr 112 114 TTA TAC CAA TTT CTC TTC CTA GCT ACT TTC ATC AAA ACA AAA ACT 119 Ser Asp Ile Lys Asn Val Asp Pro Lys Ser Phe Lys Leu Val Gln Asn 120 120 125 120 125 120 127 128 AGG GAT ATT AAG ACC GAT ATA ATC TCT TTT AGC GCA AGG GAT AGA ACA 120 121 Lys Tyr Leu Gly Val Ile Ile Gln Cys Leu Val Thr Glu Thr Lys Thr 121 122 AAG TAT CGG GAG GTA ATA ATC CTC TTT TTT AGC GCA AGG GTA AGG ACC ATC GAT 121 Lys Tyr Leu Gly Val Ile Ile Gln Cys Leu Val Thr Glu Thr Lys Thr 121 122 AAG TAT CGG AGG CAA ATA ATC CTC TTT TTT AGC GCA AGG GTA AGG ACC ATC GAT 121 Lys Tyr Leu Gly Val Ile Ile Gln Cys Leu Val Thr Glu Thr Lys Thr 122 124 126 AGC GTT AGT AGG CAC ATA TAC TTC TTT AGC GCA AGG G		
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82 GGA ACA GCA ATC AAG AGA GCC ACA TTC ATG AGC TAT AAT ACT ATC ATA 83 Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr Asn Thr Ile Ile 84 50 85 60 86 AGC AAT TGG CTG AGT TTC GAT ATT GTC AAT AAA TCA CTC CAG TTT AAA 87 Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys Ser Leu Gln Phe Lys 88 65 90 TAC AAG ACG CAA AAA GCA ACA ATT CTG GAA GCC TCA TTA AAG AAA TTG 90 TAC AAG ACG CAA AAA GCA ACA ATT CTG GAA GCC TCA TTA AAG AAA TTG 91 Tyr Lys Thr Gln Lys Ala Thr Ile Leu Glu Ala Ser Leu Lys Lys Leu 91 Tyr Lys Thr Gln Lys Ala Thr Ile Ile Pro Tyr Tyr Gly Gln Lys His 90 90 91 92 92 93 94 ATT CCT GCT TGG GAA TTA ACA ATT ATT CCT TAC TAT GGA CAA AAA CAT 95 Ile Pro Ala Trp Glu Phe Thr Ile Ile Pro Tyr Tyr Gly Gln Lys His 100 96 CAA TCT GAT ATC ACT GAT ATT GTA AGT AGT TG CAA TTA CAG TTC GAA 99 Gln Ser Asp Ile Thr Asp Ile Val Ser Ser Leu Gln Leu Gln Phe Glu 100 115 120 100 115 120 120 125 120 121 120 125 120 125 120 124 130 Ser Ser Glu Glu Ala Asp Lys Gly Asn Ser His Ser Lys Lys Met Leu 120 121 120 120 125 120 120 120 120 125 120 120 120 125 120 120 125 120 120 120 125 120 120 120 120 120 120 120 120 120 120		
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86 AGC AAT TCG CTG AGT TTC GAT ATT GTC AAT AAA TCA CTC CAG TTT AAA 240 86 AGC AAT TCG CTG AGT TTC GAT ATT GTC AAT AAA TCA CTC CAG TTT AAA 240 87 Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys Ser Leu Gln Phe Lys 80 75 80 75 80 75 80 75 80 75 80 75 80 75 80 80 75 80 75 80 75 80 75 80 75 80 75 80 75 80 75 80 80 75 80 75 80 80 75 80 80 75 80 80 75 80 80 75 80 80 75 80 80 80 75 80 80 80 80 80 80 80 80 80 80 80 80 80	82 GGA ACA GCA ATC AAG AGA GCC ACA IIO ME Ser Tyr Asn Thr Il	e Ile
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94 ATT CCT GCT TGG GAA TTT ACA ATT ATT CCT TAC TAT GGA CAA AAA CAT 95 Ile Pro Ala Trp Glu Phe Thr Ile Ile Pro Tyr Tyr Gly Gln Lys His 100 100 110 105 110 110 110 110 110 110	90 TAC AAG ACG CAA AAA GCA NON HILL Leu Glu Ala Ser Leu Lys Ly	s Leu .
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95 Ile Pro Ala Trp Glu Phe Thr The Tre Tro 105	92 AUT AUT AUT AUT COT TAC TAT GGA CAA AA	A CAT 336
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	GCC	GTG	GCC	AGG	ACA	ACG	TAT	ACT	CAT	CAG	ATA	ACA	GCA	ATA	CCT	GAT Asp	1030
155	Ala	Val	Ala	Arg	Thr	Thr	Tyr	Thr	HIS	GIII	Ile	Thr	Ala	110		Asp	
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158	CAC	TAC	TTC	GCA	CTA	GTT	TCT	CGG	TAC	TAT	GCA	TAT	GAI	Dro	Tle	TCA Ser	
159	His	Tyr	Phe	Ala	Leu	Val	Ser	Arg	TAT	Tyr	Ala	тут	365		, 110	Ser	
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188 (D) TOPOLOGY: linear 190 (ii) MOLECULE TYPE: protein																	
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273 420 275 (2) INFORMATION FOR SEQ ID NO: 3: 277 (i) SEQUENCE CHARACTERISTICS: 278 (A) LENGTH: 34 base pairs 279 (B) TYPE: nucleic acid 280 (C) STRANDEDNESS: single 281 (D) TOPOLOGY: linear 283 (ii) MOLECULE TYPE: DNA (genomic) 287 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3: 289 GAAGTTCCTA TTCTCTAGAA AGTATAGGAA CTTC 291 (2) INFORMATION FOR SEQ ID NO: 4: 293 (i) SEQUENCE CHARACTERISTICS: 294 (A) LENGTH: 68 base pairs 295 (B) TYPE: nucleic acid 296 (C) STRANDEDNESS: single 297 (D) TOPOLOGY: linear	34
297 (ii) MOLECULE TYPE: DNA (genomic) 303 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4: 305 GATCCCGGGC TACCATGGAG AAGTTCCTAT TCCGAAGTTC CTATTCTCTA GAAAGTATAG 307 GAACTTCA	60 68

VERIFICATION SUMMARY

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